

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/774, 176A
Source: IFW/6
Date Processed by STIC: 02/22/2007

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 02/22/2007

PATENT APPLICATION: US/10/774,176A

TIME: 13:25:35

Input Set : N:\efs\02_22_07\10774176A_efs\021911-000510US.txt

Output Set: N:\CRF4\02222007\J774176A.raw

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3 <110> APPLICANT: OXFORD BIOMEDICA (UK) LTD.
4     CARROLL, MILES WILLIAM
5     MYERS, KEVIN ALAN
7 <120> TITLE OF INVENTION: POLYPEPTIDE
9 <130> FILE REFERENCE: 021911-000510US
11 <140> CURRENT APPLICATION NUMBER: 10/774,176A
12 <141> CURRENT FILING DATE: 2004-02-06
14 <150> PRIOR APPLICATION NUMBER: 09/533,798
15 <151> PRIOR FILING DATE: 2000-03-24
17 <150> PRIOR APPLICATION NUMBER: 60/126,187
18 <151> PRIOR FILING DATE: 1999-03-25
20 <150> PRIOR APPLICATION NUMBER: 60/126,188
21 <151> PRIOR FILING DATE: 1999-03-25
23 <150> PRIOR APPLICATION NUMBER: GB 9825303.2
24 <151> PRIOR FILING DATE: 1998-11-18
26 <150> PRIOR APPLICATION NUMBER: GB 9901739.4
27 <151> PRIOR FILING DATE: 1999-01-27
29 <150> PRIOR APPLICATION NUMBER: GB 9917995.4
30 <151> PRIOR FILING DATE: 1999-07-30
32 <160> NUMBER OF SEQ ID NOS: 27
34 <170> SOFTWARE: PatentIn version 2.1
36 <210> SEQ ID NO: 1
37 <211> LENGTH: 1263
38 <212> TYPE: DNA
39 <213> ORGANISM: Homo sapiens
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44 ctagecgtgg tactcctggg ctgggtctcc tgcgtctctc ccacctctc ggcatcctcc      120
46 ttctcctcct cggcgccggt cctggcttcc gccgtgtccg cccagccccc gctgccggac      180
48 cagtgcctcg cgtgtgcgga gtgctccgag gcagcgcgca cagtcaagtg cgttaaccgc      240
50 aatctgaccg aggtgccac ggacctgcc gcctacgtgc gcaacctctt ccttaccggc      300
52 aaccagctgg cgtgctccc tgcggcgcc ttgcggcgcc ggccgcccgt ggccggagctg      360
54 gccgcgtca acctcagcgg cagccgcctg gacgaggtgc gcgcgggcgc cttcgagcat      420
56 ctgccagacc tgcgccagct cgacctcagc cacaacctac tggccgacct cagtccttcc      480
58 gctttctcgg gcagcaatgc cagcgtctcg gccccagtc cccttggtgga actgatcctg      540
60 aaccacatcg tccccctga agatgagcgg cagaaccgga gcttcgaggg catggtggtg      600
62 gcggccctgc tggcgggccc tgcactgcag gggctccgcc gcttgagact ggccagcaac      660
64 cacttccttt acctgccgcg ggatgtgctg gcccaactgc ccagcctcag gcacctggac      720
66 ttaagtaata attcgtggt gagcctgacc tacgtgtcct tccgcaacct gacacatcta      780
68 gaaagcctcc acctggagga caatgccctc aaggtccttc acaatggcac cctggctgag      840
70 ttgcaaggte taccacacat tagggttttc ctggacaaca atccctgggt ctgcgactgc      900
72 cacatggcag acatggtgac ctggctcaag gaaacagagg tagtgcaggg caaagaccgg      960
74 ctcacctgtg catatccgga aaaaatgagg aatcgggtcc tcttggaact caacagtgtc     1020

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76 gacctggact gtgaccgat ttttccccca tccctgcaaa cctcttatgt cttcctgggt 1080
78 attgttttag cctgatagg cgctattttc ctcctgggtt tgtatttgaa ccgcaagggg 1140
80 ataaaaaagt ggatgcataa catcagagat gcctgcaggg atcacatgga agggatatcat 1200
82 tacagatatg aaatcaatgc ggaccccaga ttaacaaacc tcagttctaa ctcgggatgtc 1260
84 tga 1263
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88 <211> LENGTH: 1281
89 <212> TYPE: DNA
90 <213> ORGANISM: Mus musculus
92 <400> SEQUENCE: 2
93 atgcctgggg cgggctccc gggcccctcc gccggggacg gacggctgag gttggcaagg 60
95 ctggcgctag tgetgctggg ttgggtctcc ggcgcggccc ccagctcttc ggtaccctcg 120
97 ttttccacct ccccggcaga cttcctggcc tcggggtctg cgcagcctcc gccagccgag 180
99 agatgccccg cggcgtgcga gtgctccgag gccggcgcca cggttaagtg cgtgaaccgc 240
101 aacctgctgg aggtgccggc ggatctaccg ccttacgtgc gcaacctttt ccttacccgc 300
103 aaccagatga ccgtgctccc cgcggggccc ttgcggcgcc agccgcgcgt cgcgcacctg 360
105 gaggcgctca acctcagcgg caaccacctg aaggagggtg gtgcagggtg cttcgagcat 420
107 ctgccgggtc tgcgcgggtc tgacctcagc cacaacctc tcaccaacct cagcgccctc 480
109 gtctttgcgg gcagcaacgc cagcgtctcg gccccagcc ccctggagga gctgatcctg 540
111 aatcacatcg tccccctga ggatcagagg cagaacggga gcttcgaggg tatggtggcc 600
113 ttogaaggca tgggtggcagc agctctgcgc tcaggccttg cactccgagg tcttacacgc 660
115 ctggagctag ccagcaatca ctttcttttc ctgcctcggg acttactagc ccaactgccg 720
117 agtctcagat acctggacct caggaacaat tccttggtga gcctgacct cgcaccttc 780
119 cgcaacctga cacacctga aagcctccac ttggaggaca atgcccctca ggctccttcac 840
121 aactccacct tggctgagtg gcaaggcctg gctcatgtca aggtgttccg ggacaacaat 900
123 ccctgggttt gcgactgcta catggctgac atgggtggctt ggcttaaaga gacagagggtg 960
125 gtgccagata aagccaggct tacctgcgca ttcccggaga agatgaggaa tcgtggcctc 1020
127 ttagacctca acagctctga cctggactgt gacgtgtcc ttcccgaatc cctgcagact 1080
129 tcctatgtct tcctaggtat tgttttagct ctgataggcg ctattttcct cctcgttttg 1140
131 tatttgaaac gtaaaggcat aaaaaagtgg atgcataaca tcagagatgc ctgcagggat 1200
133 cacatggaag ggtatcatta cagatacga atcaatgcgg accccagatt aacaaatctt 1260
135 agttccaact cggatgtctg a 1281
138 <210> SEQ ID NO: 3
139 <211> LENGTH: 901
140 <212> TYPE: DNA
141 <213> ORGANISM: Canis sp.
143 <220> FEATURE:
144 <221> NAME/KEY: modified_base
145 <222> LOCATION: (66)
146 <223> OTHER INFORMATION: a, c, g or t
148 <220> FEATURE:
149 <221> NAME/KEY: modified_base
150 <222> LOCATION: (145)
151 <223> OTHER INFORMATION: a, c, g or t
153 <220> FEATURE:
154 <221> NAME/KEY: modified_base
155 <222> LOCATION: (277)..(278)
156 <223> OTHER INFORMATION: a, c, g or t
158 <220> FEATURE:

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160 <222> LOCATION: (287)
161 <223> OTHER INFORMATION: a, c, g or t
163 <220> FEATURE:
164 <221> NAME/KEY: modified_base
165 <222> LOCATION: (353)
166 <223> OTHER INFORMATION: a, c, g or t
168 <220> FEATURE:
169 <221> NAME/KEY: modified_base
170 <222> LOCATION: (358)
171 <223> OTHER INFORMATION: a, c, g or t
174 <220> FEATURE:
175 <221> NAME/KEY: modified_base
176 <222> LOCATION: (428)..(429)
177 <223> OTHER INFORMATION: a, c, g or t
179 <220> FEATURE:
180 <221> NAME/KEY: modified_base
181 <222> LOCATION: (577)
182 <223> OTHER INFORMATION: a, c, g or t
184 <220> FEATURE:
185 <221> NAME/KEY: modified_base
186 <222> LOCATION: (580)
187 <223> OTHER INFORMATION: a, c, g or t
189 <220> FEATURE:
190 <221> NAME/KEY: modified_base
191 <222> LOCATION: (719)
192 <223> OTHER INFORMATION: a, c, g or t
194 <220> FEATURE:
195 <221> NAME/KEY: modified_base
196 <222> LOCATION: (788)
197 <223> OTHER INFORMATION: a, c, g or t
199 <220> FEATURE:
200 <221> NAME/KEY: modified_base
201 <222> LOCATION: (863)
202 <223> OTHER INFORMATION: a, c, g or t
204 <220> FEATURE:
205 <221> NAME/KEY: modified_base
206 <222> LOCATION: (868)
207 <223> OTHER INFORMATION: a, c, g or t
209 <220> FEATURE:
210 <221> NAME/KEY: modified_base
211 <222> LOCATION: (871)
212 <223> OTHER INFORMATION: a, c, g or t
214 <400> SEQUENCE: 3
215 atcgtgcccc ccgacgaccg gcggcagaac cggagcttcg aggtcatggt ggcggctgcc      60
W--> 217 vddrrnrsvm vaaactccga gcgggccgcg cgcttcgcgg gctgcagtgc ctggagctgg      120
219 ccggcaaccg cttragrgr gcagnrctct acttgectcg cgacgtctcg gccagctac      180
221 ccggcctccg gcacctggac ctgcgcyrdrv agrhdraaca attccctggg gacgctcacc      240
223 tacgtgtcct tccgcaacct gacgcacttg gagagcnnsv styvsrnths ctccacctgg      300

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225 aggacaacgc cctcaaggctc cttcacaacg ccaccctggc ggagctgcag hdnakvhnat 360
227 aagcctgccc cacgtccggg tcttcctgga caacaacccc tgggtctgcg attgtcacat 420
229 gshvrvdnnw vcdchmgcag acatgggtggc ctgggtcaag gagacagagg tgggtgccggg 480
231 caaagccggg ctcaccadm vawktvvgkag ttgtgcattc ccggagaaaa tgaggaatcg 540
233 ggccctcttg gaactcaaca gctcccacct gcakmrnran sshgactgtg accctatcct 600
235 ccctccatcc ctgcagactt cttatgtctt cctaggtatt gtdcdstsy vgvttagccc 660
237 tgataggcgc catcttccta ctggttttgt atttgaaccg caaggggata aagagavynr 720
239 kgkaagtgga tgcataacat cagagatgcc tgcagggatc acatggaagg gtatcactac 780
241 agakwmhnr dacr dhmg yhy rtac gaaatc aatgcagacc ccaggttaac aaacctcagt 840
243 tccaattcgg atgtctgaga aynadrtnss nsdvacagtc ggggacagac caaggacaac 900
245 t 901

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248 <210> SEQ ID NO: 4

249 <211> LENGTH: 238

250 <212> TYPE: PRT

251 <213> ORGANISM: Canis sp.

253 <400> SEQUENCE: 4

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254 Ile Val Pro Pro Asp Asp Arg Arg Gln Asn Arg Ser Phe Glu Val Met
255 1 5 10 15
257 Val Ala Ala Ala Leu Arg Ala Gly Arg Ala Leu Arg Gly Leu Gln Cys
258 20 25 30
260 Leu Glu Leu Ala Gly Asn Arg Phe Leu Tyr Leu Pro Arg Asp Val Leu
261 35 40 45
263 Ala Gln Leu Pro Gly Leu Arg His Leu Asp Leu Arg Asn Asn Ser Leu
264 50 55 60
266 Val Ser Leu Thr Tyr Val Ser Phe Arg Asn Leu Thr His Leu Glu Ser
267 65 70 75 80
269 Leu His Leu Glu Asp Asn Ala Leu Lys Val Leu His Asn Ala Thr Leu
270 85 90 95
272 Ala Glu Leu Gln Ser Leu Pro His Val Arg Val Phe Leu Asp Asn Asn
273 100 105 110
275 Pro Trp Val Cys Asp Cys His Met Ala Asp Met Val Ala Trp Leu Lys
276 115 120 125
278 Glu Thr Glu Val Val Pro Gly Lys Ala Gly Leu Thr Cys Ala Phe Pro
279 130 135 140
281 Glu Lys Met Arg Asn Arg Ala Leu Leu Glu Leu Asn Ser Ser His Leu
282 145 150 155 160
284 Asp Cys Asp Pro Ile Leu Pro Pro Ser Leu Gln Thr Ser Tyr Val Phe
285 165 170 175
287 Leu Gly Ile Val Leu Ala Leu Ile Gly Ala Ile Phe Leu Leu Val Leu
288 180 185 190
290 Tyr Leu Asn Arg Lys Gly Ile Lys Lys Trp Met His Asn Ile Arg Asp
291 195 200 205
293 Ala Cys Arg Asp His Met Glu Gly Tyr His Tyr Arg Tyr Glu Ile Asn
294 210 215 220
296 Ala Asp Pro Arg Leu Thr Asn Leu Ser Ser Asn Ser Asp Val
297 225 230 235

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300 <210> SEQ ID NO: 5

301 <211> LENGTH: 9

302 <212> TYPE: PRT

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Input Set : N:\efs\02_22_07\10774176A_efs\021911-000510US.txt

Output Set: N:\CRF4\02222007\J774176A.raw

303 <213> ORGANISM: Artificial Sequence
305 <220> FEATURE:
306 <223> OTHER INFORMATION: Description of Artificial Sequence: 5T4 9 Mer
308 <400> SEQUENCE: 5
309 Phe Leu Thr Gly Asn Gln Leu Ala Val
310 1 5
313 <210> SEQ ID NO: 6
314 <211> LENGTH: 9
315 <212> TYPE: PRT
316 <213> ORGANISM: Artificial Sequence
318 <220> FEATURE:
319 <223> OTHER INFORMATION: Description of Artificial Sequence: 5T4 9 Mer
321 <400> SEQUENCE: 6
322 Ala Leu Ile Gly Ala Ile Phe Leu Leu
323 1 5
326 <210> SEQ ID NO: 7
327 <211> LENGTH: 9
328 <212> TYPE: PRT
329 <213> ORGANISM: Artificial Sequence
331 <220> FEATURE:
332 <223> OTHER INFORMATION: Description of Artificial Sequence: 5T4 9 Mer
334 <400> SEQUENCE: 7
335 Ser Leu Gln Thr Ser Tyr Val Phe Leu
336 1 5
339 <210> SEQ ID NO: 8
340 <211> LENGTH: 9
341 <212> TYPE: PRT
342 <213> ORGANISM: Artificial Sequence
344 <220> FEATURE:
345 <223> OTHER INFORMATION: Description of Artificial Sequence: 5T4 9 Mer
347 <400> SEQUENCE: 8
348 Ala Ile Phe Leu Leu Val Leu Tyr Leu
349 1 5
352 <210> SEQ ID NO: 9
353 <211> LENGTH: 9
354 <212> TYPE: PRT
355 <213> ORGANISM: Artificial Sequence
357 <220> FEATURE:
358 <223> OTHER INFORMATION: Description of Artificial Sequence: 5T4 9 Mer
360 <400> SEQUENCE: 9
361 Gly Leu Pro His Ile Arg Val Phe Leu
362 1 5
365 <210> SEQ ID NO: 10
366 <211> LENGTH: 9
367 <212> TYPE: PRT
368 <213> ORGANISM: Artificial Sequence
370 <220> FEATURE:
371 <223> OTHER INFORMATION: Description of Artificial Sequence: 5T4 9 Mer
373 <400> SEQUENCE: 10

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/774,176A

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Input Set : N:\efs\02_22_07\10774176A_efs\021911-000510US.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 66,145,277,278,287,353,358,428,429,577,580,719,788,863,868

Seq#:3; N Pos. 871

VERIFICATION SUMMARY

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L:217 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:60

M:341 Repeated in SeqNo=3